

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/086,427DATE: 08/03/93
TIME: 16:04:18

INPUT SET: S1157.raw

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Gospodarowicz, Denis
Masiarz, Frank R.(ii) TITLE OF INVENTION: A Truncated Keratinocyte Growth Factor
(KGF) Having Increased Biological Activity

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Chiron Corporation
(B) STREET: 4560 Horton Street
(C) CITY: Emeryville
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94608

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Amy L. Collins, Esq.
(B) REGISTRATION NUMBER: 33,370
(C) REFERENCE/DOCKET NUMBER: 0953.001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (510) 601-2768
(B) TELEFAX: (510) 655-3542

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	His	Lys	Trp	Ile	Leu	Thr	Trp	Ile	Leu	Pro	Thr	Leu	Leu	Tyr	Arg
1				5					10					15	
Ser	Cys	Phe	His	Ile	Ile	Cys	Leu	Val	Gly	Thr	Ile	Ser	Leu	Ala	Cys
			20					25					30		
Asn	Asp	Met	Thr	Pro	Glu	Gln	Met	Ala	Thr	Asn	Val	Asn	Cys	Ser	Ser
		35					40					45			
Pro	Glu	Arg	His	Thr	Arg	Ser	Tyr	Asp	Tyr	Met	Glu	Gly	Gly	Asp	Ile
	50					55					60				
Arg	Val	Arg	Arg	Leu	Phe	Cys	Arg	Thr	Gln	Trp	Tyr	Leu	Arg	Ile	Asp
65				70					75					80	
Lys	Arg	Gly	Lys	Val	Lys	Gly	Thr	Gln	Glu	Met	Lys	Asn	Asn	Tyr	Asn
			85					90						95	
Ile	Met	Glu	Ile	Arg	Thr	Val	Ala	Val	Gly	Ile	Val	Ala	Ile	Lys	Gly
		100					105					110			
Val	Glu	Ser	Glu	Phe	Tyr	Leu	Ala	Met	Asn	Lys	Glu	Gly	Lys	Leu	Tyr
		115					120					125			
Ala	Lys	Lys	Glu	Cys	Asn	Glu	Asp	Cys	Asn	Phe	Lys	Glu	Leu	Ile	Leu
	130					135					140				
Glu	Asn	His	Tyr	Asn	Thr	Tyr	Ala	Ser	Ala	Lys	Trp	Thr	His	Asn	Gly
145					150					155				160	
Gly	Glu	Met	Phe	Val	Ala	Leu	Asn	Gln	Lys	Gly	Ile	Pro	Val	Arg	Gly
			165					170					175		
Lys	Lys	Thr	Lys	Lys	Glu	Gln	Lys	Thr	Ala	His	Phe	Leu	Pro	Met	Ala
			180					185					190		
Ile	Thr														

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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103 (ii) MOLECULE TYPE: protein

104

105

106

107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

108

109 Cys Asn Asp Met Thr Pro Glu Gln Met Ala Thr Asn Val Asn Cys Ser

110 1 5 10 15

111

112 Ser Pro Glu Arg His Thr Arg

113 20

114

115 (2) INFORMATION FOR SEQ ID NO:3:

116

117 (i) SEQUENCE CHARACTERISTICS:

118 (A) LENGTH: 6 amino acids

119 (B) TYPE: amino acid

120 (C) STRANDEDNESS: single

121 (D) TOPOLOGY: linear

122

123 (ii) MOLECULE TYPE: peptide

124

125

126

127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

128

129 Met His Lys Trp Ile Leu

130 1 5

131

132 (2) INFORMATION FOR SEQ ID NO:4:

133

134 (i) SEQUENCE CHARACTERISTICS:

135 (A) LENGTH: 35 base pairs

136 (B) TYPE: nucleic acid

137 (C) STRANDEDNESS: single

138 (D) TOPOLOGY: linear

139

140 (ii) MOLECULE TYPE: DNA (genomic)

141

142

143

144 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

145

146 AGATCTCTGC AGCTATAATG CACAAATGGA TACTG

35

147

148 (2) INFORMATION FOR SEQ ID NO:5:

149

150 (i) SEQUENCE CHARACTERISTICS:

151 (A) LENGTH: 7 amino acids

152 (B) TYPE: amino acid

153 (C) STRANDEDNESS: single

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154 (D) TOPOLOGY: linear

155

156 (ii) MOLECULE TYPE: peptide

157

158

159

160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

161

162 Thr Ile Ala Met Pro Leu Phe

163

1

5

164

165 (2) INFORMATION FOR SEQ ID NO:6:

166

167 (i) SEQUENCE CHARACTERISTICS:

168 (A) LENGTH: 38 base pairs

169 (B) TYPE: nucleic acid

170 (C) STRANDEDNESS: single

171 (D) TOPOLOGY: linear

172

173 (ii) MOLECULE TYPE: DNA (genomic)

174

175

176

177 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

178

179 AGATCTGCGG CCGCTTAAGT TATTGCCATA GGAAGAAA

38

180

181 (2) INFORMATION FOR SEQ ID NO:7:

182

183 (i) SEQUENCE CHARACTERISTICS:

184 (A) LENGTH: 20 amino acids

185 (B) TYPE: amino acid

186 (C) STRANDEDNESS: single

187 (D) TOPOLOGY: linear

188

189 (ii) MOLECULE TYPE: peptide

190

191

192

193 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

194

195 Ser Tyr Asp Tyr Met Glu Gly Gly Asp Ile Arg Val Arg Arg Leu Phe

196

1

5

10

15

197

198 Xaa Arg Thr Gln

199

20

200

201 (2) INFORMATION FOR SEQ ID NO:8:

202

203 (i) SEQUENCE CHARACTERISTICS:

204 (A) LENGTH: 32 base pairs

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205 (B) TYPE: nucleic acid
206 (C) STRANDEDNESS: single
207 (D) TOPOLOGY: linear
208
209 (ii) MOLECULE TYPE: DNA (genomic)
210
211
212
213 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
214
215 GGTGGTGGAT CCCCAGCTTA GTTCATAGGT CC 32
216
217 (2) INFORMATION FOR SEQ ID NO:9:
218
219 (i) SEQUENCE CHARACTERISTICS:
220 (A) LENGTH: 12 amino acids
221 (B) TYPE: amino acid
222 (C) STRANDEDNESS: single
223 (D) TOPOLOGY: linear
224
225 (ii) MOLECULE TYPE: peptide
226
227
228
229 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
230
231 His Gln Asn Val Phe Arg Lys Ala Pro Ile Gln Ala
232 1 5 10
233
234 (2) INFORMATION FOR SEQ ID NO:10:
235
236 (i) SEQUENCE CHARACTERISTICS:
237 (A) LENGTH: 36 base pairs
238 (B) TYPE: nucleic acid
239 (C) STRANDEDNESS: single
240 (D) TOPOLOGY: linear
241
242 (ii) MOLECULE TYPE: DNA (genomic)
243
244
245
246 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
247
248 GTGTTGGTTA ACGAATCGCT TAGCCGGAAT TTGTGC 36
249
250 (2) INFORMATION FOR SEQ ID NO:11:
251
252 (i) SEQUENCE CHARACTERISTICS:
253 (A) LENGTH: 12 amino acids
254 (B) TYPE: amino acid
255 (C) STRANDEDNESS: single

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256 (D) TOPOLOGY: linear
257
258 (ii) MOLECULE TYPE: peptide
259
260
261
262 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
263
264 Pro Ala Lys Arg Ser Tyr Asp Tyr Met Glu Gly Gly
265 1 5 10
266
267 (2) INFORMATION FOR SEQ ID NO:12:
268
269 (i) SEQUENCE CHARACTERISTICS:
270 (A) LENGTH: 39 base pairs
271 (B) TYPE: nucleic acid
272 (C) STRANDEDNESS: single
273 (D) TOPOLOGY: linear
274
275 (ii) MOLECULE TYPE: DNA (genomic)
276
277
278
279 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
280
281 CCGCCGGCTA AGCGAAGTTA TGATTACATG GAAGGAGGG
282
283 (2) INFORMATION FOR SEQ ID NO:13:
284
285 (i) SEQUENCE CHARACTERISTICS:
286 (A) LENGTH: 8 amino acids
287 (B) TYPE: amino acid
288 (C) STRANDEDNESS: single
289 (D) TOPOLOGY: linear
290
291 (ii) MOLECULE TYPE: peptide
292
293
294
295 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
296
297 Thr Ile Ala Met Pro Leu Phe His
298 1 5
299
300 (2) INFORMATION FOR SEQ ID NO:14:
301
302 (i) SEQUENCE CHARACTERISTICS:
303 (A) LENGTH: 39 base pairs
304 (B) TYPE: nucleic acid
305 (C) STRANDEDNESS: single
306 (D) TOPOLOGY: linear

39

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307
308 (ii) MOLECULE TYPE: DNA (genomic)
309
310
311
312 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
313
314 GGTGGTGTCTG ACTTAAGTTA TTGCCATAGG AAGAAAGTG 39
315
316 (2) INFORMATION FOR SEQ ID NO:15:
317
318 (i) SEQUENCE CHARACTERISTICS:
319 (A) LENGTH: 25 base pairs
320 (B) TYPE: nucleic acid
321 (C) STRANDEDNESS: single
322 (D) TOPOLOGY: linear
323
324 (ii) MOLECULE TYPE: DNA (genomic)
325
326
327
328 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
329
330 GATCAGATCT AAATTTCCCG GATCC 25
331
332 (2) INFORMATION FOR SEQ ID NO:16:
333
334 (i) SEQUENCE CHARACTERISTICS:
335 (A) LENGTH: 25 base pairs
336 (B) TYPE: nucleic acid
337 (C) STRANDEDNESS: single
338 (D) TOPOLOGY: linear
339
340 (ii) MOLECULE TYPE: DNA (genomic)
341
342
343
344 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:
345
346 TCTAGATTTA AAGGCCTAG GAGCT 25
347
348 (2) INFORMATION FOR SEQ ID NO:17:
349
350 (i) SEQUENCE CHARACTERISTICS:
351 (A) LENGTH: 9 amino acids
352 (B) TYPE: amino acid
353 (C) STRANDEDNESS: single
354 (D) TOPOLOGY: linear
355
356 (ii) MOLECULE TYPE: DNA (genomic)
357

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358

359

360 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

361

362 Met Ser Tyr Asp Tyr Met Glu Gly Gly

363 1 5

364

365 (2) INFORMATION FOR SEQ ID NO:18:

366

367 (i) SEQUENCE CHARACTERISTICS:

368 (A) LENGTH: 35 base pairs

369 (B) TYPE: nucleic acid

370 (C) STRANDEDNESS: single

371 (D) TOPOLOGY: linear

372

373 (ii) MOLECULE TYPE: DNA (genomic)

374

375

376

377 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

378

379 GTTGTTTCAT GAGTTATGAT TACATGGAAG GAGGG

35

380

381

382 (2) INFORMATION FOR SEQ ID NO:19:

383

384 (i) SEQUENCE CHARACTERISTICS:

385 (A) LENGTH: 99 base pairs

386 (B) TYPE: nucleic acid

387 (C) STRANDEDNESS: single

388 (D) TOPOLOGY: linear

389

390 (ii) MOLECULE TYPE: DNA (genomic)

391

392

393 (ix) FEATURE:

394 (A) NAME/KEY: -

395 (B) LOCATION: 13..14

396 (D) OTHER INFORMATION: /note= "The figure did not contain
397 the intervening polyhedrin sequences."

398

399 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

400

401 TATAAATATT CCGGGCGCGG ATCGGTACCA GATCTGCAGA ATTCTAGAGG ATCCTGATCA 60

402

403 GCTAGCAGAG CTCGCGGCCG CCCGGGCCGT ACCGACTCT

99

404

405

406

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/086,427

DATE: 08/03/93
TIME: 16:04:50

INPUT SET: S1157.raw

Line	Error	Original Text
29	Wrong Filing Date	(B) FILING DATE:

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/08/086,427

DATE: 08/03/93
TIME: 16:04:51

INPUT SET: S1157.raw

APPLICATION NUMBER
FILING DATE
PRIOR APPLICATION DATA

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/08/086,427

DATE: 08/03/93
TIME: 16:04:51

INPUT SET: S1157.raw

Line

Original Text

Corrected Text

CRF Errors Corrected by the STIC Systems Branch

C 12

Serial Number: 081086, 427

CRF Processing Date: 8/3/93
 Edited by: [Signature]
 Verified by: [Signature] (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☒ Changed the margins in cases where the sequence text was "wrapped" down to the next line. *Just seq 19 (P-8)*
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Inserted a space between the last nucleic designator and the nucleic number for sequences: _____
- ☐ Deleted page numbers in the text of the sequence listing, which is considered invalid text.
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☐ Deleted non-ASCII "garbage" at the end of files, and other invalid text, such as a secretary's initials.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

8/01/93